0450 OIPE #2

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 10/047,593 **ENTERED**

CRF Processing Date: 2/14/2002
Edited by: _____ A
Verified by: _____ A _____ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☑ Other: _Inserted hard returns globally_ _____

*Examiner: **The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.** 3/1/95

OIPE

RAW SEQUENCE LISTING   DATE: 02/14/2002
PATENT APPLICATION: US/10/047,593   TIME: 20:21:33

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02142002\J047593.raw

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   4 <110> APPLICANT: Crane, Edmund H. III
   5        Rice, Douglas A.
   7 <120> TITLE OF INVENTION: Maize NPR1 Polynucleotides and Methods
   8        of Use
  10 <130> FILE REFERENCE: 1090D2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/047,593
C--> 12 <141> CURRENT FILING DATE: 2002-01-15
  12 <150> PRIOR APPLICATION NUMBER: 60/130,692
  13 <151> PRIOR FILING DATE: 1999-04-23
  15 <150> PRIOR APPLICATION NUMBER: 09/551,778
  16 <151> PRIOR FILING DATE: 2000-04-18
  18 <160> NUMBER OF SEQ ID NOS: 6
  20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 2154
  24 <212> TYPE: DNA
  25 <213> ORGANISM: Zea mays
  27 <220> FEATURE:
  28 <221> NAME/KEY: CDS
  29 <222> LOCATION: (67)...(1929)
  31 <221> NAME/KEY: 3'UTR
  32 <222> LOCATION: (1933)...(2154)
  34 <221> NAME/KEY: 5'UTR
  35 <222> LOCATION: (1)...(66)
  37 <400> SEQUENCE: 1
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  39 gaagcc atg gag ccg tcg tcg tcc atc acg ttc gcg tcg tcg tcg tcg    108
  40        Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser
  41         1               5                       10
  43 tac ctg tcc aac ggc tcg agc ccc tgt tcc gtc gcg ctg ccg ccg cca   156
  44 Tyr Leu Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro
  45  15                  20                  25                  30
  47 ggg ccg ccc cag act ccc ccg ttg cct gcc ggc cag ggg tgg ggt ggt   204
  48 Gly Pro Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly
  49                  35                  40                  45
  51 gga gtc gct gcc gca ggg agc gga ggc agc gtg gag gcc gtg agc ctg   252
  52 Gly Val Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu
  53              50                  55                  60
  55 aac cgg ctc agc aaa aac ctc gag cgg ctg ctc ctc gac ccg gac cta   300
  56 Asn Arg Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu
  57              65                  70                  75
  59 gac tgc agc gac gcc gac gtc gat gtg ccc gac ggt ggg ccg ccc gta   348
  60 Asp Cys Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val
```

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02142002\J047593.raw

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61      80                      85                      90
63 ccc atc cac cgc tgc atc ctt gcc gca cgc agc gac ttc ttc tac gac    396
64 Pro Ile His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp
65 95                  100                 105                 110
67 ctc ttc gcc gct cgc ggc cgc gca ggg gca gcg cgc ggt gat gcg gcc    444
68 Leu Phe Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala
69                 115                 120                 125
71 gcc ggc gcc gga gta gcc gcg gag ggg gct gcc agt gga agg ccg cgg    492
72 Ala Gly Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg
73                 130                 135                 140
75 tac aag atg gag gat ctc gtt ccc gcc ggc cgc gtg ggg cgc gag gcc    540
76 Tyr Lys Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala
77         145                 150                 155
79 ttc cag gcg ttt ctg ggg tac ctg tac acc ggc aag ctc cgg ccg gca    588
80 Phe Gln Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala
81         160                 165                 170
83 ccg gtc gac gtg gtg tct tgt gct gac cca gtg tgc cat cac gat tcg    636
84 Pro Val Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser
85 175                 180                 185                 190
87 tgc ccg ccg gcc atc agg tcc gcg gtc gag ctc atg tac gcg gcg tgt    684
88 Cys Pro Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys
89                 195                 200                 205
91 acc ttc aag atc ccc gag ctc acc tcg ctc ttc cag cgc cgg ctt ctt    732
92 Thr Phe Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu
93         210                 215                 220
95 aat ttt gta gac aag act cta gtg gag gat gtt att cct att ctg gaa    780
96 Asn Phe Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu
97.        225                 230                 235
99 gtt gct tcc cac tca ggg ctg act caa gtg atc gac aaa tgt att caa    828
100 Val Ala Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln
101         240                 245                 250
103 agg att gct aga tca gat ctc gac gat ata tct ttg gat aag gag ctc    876
104 Arg Ile Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu
105 255                 260                 265                 270
107 cct cca gaa gca gtt gat gag ata aaa aat ttg cgc aag aag tca caa    924
108 Pro Pro Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln
109                 275                 280                 285
111 act gct gat ggt gat acg ttc att tcg gac cct gtg cat gag aaa aga    972
112 Thr Ala Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg
113                 290                 295                 300
115 gtc aga aga atc cac agg gca ctt gac tct gat gat gtt gag ctt gtg    1020
116 Val Arg Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val
117         305                 310                 315
119 aag ttg ctt ctt aat gag tcc gac atc aca tta gat gat gcc aac gca    1068
120 Lys Leu Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala
121         320                 325                 330
123 tta cac tat gct gct tct tac tgt gat cct aaa gtt gtc tca gag ctg    1116
124 Leu His Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu
125 335                 340                 345                 350
```

RAW SEQUENCE LISTING   DATE: 02/14/2002
PATENT APPLICATION: US/10/047,593   TIME: 20:21:33

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\02142002\J047593.raw

```
127 tta gat ttg gca atg gct aac tta aat ttg aag aat agc cgt ggg tac      1164
128 Leu Asp Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr
129             355                 360                 365
131 aca gca ctc cac ttg gct gct atg agg aga gaa cca gct ata atc atg      1212
132 Thr Ala Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met
133             370                 375                 380
135 tgt ctc ctt aac aaa ggg gca aat gtg tca caa ctg aca gct gat ggc      1260
136 Cys Leu Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly
137             385                 390                 395
139 agg agc gca att ggt att tgt cgg agg tta aca aga gca aaa gac tac      1308
140 Arg Ser Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr
141             400                 405                 410
143 aat aca aag atg gag cag ggt caa gaa tca aat aaa gat agg ctg tgt      1356
144 Asn Thr Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys
145 415                 420                 425                 430
147 ata gat att cta gag agg gag atg atg cgg aat cct atg gcg gtg gaa      1404
148 Ile Asp Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu
149             435                 440                 445
151 gat gcc gtc acc tcg cct ttg ttg gca gat gat ctt cac atg aag ctt      1452
152 Asp Ala Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu
153             450                 455                 460
155 ctc tac ctg gaa aac aga gtt gca ttt gct aga ttg ttc ttt cct gct      1500
156 Leu Tyr Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala
157             465                 470                 475
159 gaa gcc aag gtc gcc atg caa atc gca caa gca gac acc aca gaa gaa      1548
160 Glu Ala Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu
161         480                 485                 490
163 ttc ggc ggt ata gtt gca gtt gca gca agc act tct ggt aaa ctg agg      1596
164 Phe Gly Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg
165 495                 500                 505                 510
167 gag gtg gac ctt aat gag acg cca gtg aca caa aac aaa agg ctc cgt      1644
168 Glu Val Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg
169             515                 520                 525
171 tca agg gta gat gca ctg atg aaa aca gtg gag ctg ggc cgt cgg tac      1692
172 Ser Arg Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr
173             530                 535                 540
175 ttc ccg aac tgc tcg cag gtg ctg gac aag ttc ctg gag gac gat ctg      1740
176 Phe Pro Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu
177             545                 550                 555
179 ccg gaa ggt ctg gac cag ttc tac ctc cag agg ggc aca gcc gat gag      1788
180 Pro Glu Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu
181         560                 565                 570
183 cag aag gtg aag agg atg cgc ttc tgc gag ctg aaa gag gac gtg ctg      1836
184 Gln Lys Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu
185 575                 580                 585                 590
187 aag gcg ttt agc aag gac aag gcg gag ggc agc gtg ttc tcg ggc ctg      1884
188 Lys Ala Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu
189             595                 600                 605
191 tcc tcg tcg tcg tcg tgc tcg ccg ccc cag aag tat gcc cag agg          1929
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/047,593

DATE: 02/14/2002
TIME: 20:21:33

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\02142002\J047593.raw**

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192 Ser Ser Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
193             610                 615                 620
195 tgatcaaggc accagttttt gccgtatagt ttgttatcat ggtcttcgag acttggaccc  1989
196 ggacagcata tagggacatg tacacctgtg tatgtatagt gcttacaatt ggcgtaagta  2049
197 gaactatatg tatggaacat aaggaaacat ggcaggaaca ccgtgcaaaa agatgaaaag  2109
198 atggccgaag tgctctatgc gaaaaaaaaa aaaaaaaaaa aaaaa                   2154
200 <210> SEQ ID NO: 2
201 <211> LENGTH: 621
202 <212> TYPE: PRT
203 <213> ORGANISM: Zea mays
205 <400> SEQUENCE: 2
206 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser Tyr Leu
207  1               5                 10                  15
208 Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro Gly Pro
209             20                  25                  30
210 Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly Gly Val
211             35                  40                  45
212 Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu Asn Arg
213         50                  55                  60
214 Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu Asp Cys
215 65                  70                  75                  80
216 Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
217             85                  90                  95
218 His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
219             100                 105                 110
220 Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Ala Gly
221         115                 120                 125
222 Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
223         130                 135                 140
224 Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
225 145                 150                 155                 160
226 Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
227             165                 170                 175
228 Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
229             180                 185                 190
230 Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
231         195                 200                 205
232 Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
233         210                 215                 220
234 Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
235 225                 230                 235                 240
236 Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
237             245                 250                 255
238 Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
239             260                 265                 270
240 Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln Thr Ala
241         275                 280                 285
242 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
243         290                 295                 300
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244 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
245 305               310               315               320
246 Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala Leu His
247               325               330               335
248 Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp
249           340               345               350
250 Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
251       355               360               365
252 Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
253       370               375               380
254 Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
255 385               390               395               400
256 Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
257               405               410               415
258 Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
259           420               425               430
260 Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
261       435               440               445
262 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
263       450               455               460
264 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
265 465               470               475               480
266 Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
267               485               490               495
268 Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
269           500               505               510
270 Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
271       515               520               525
272 Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
273       530               535               540
274 Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
275 545               550               555               560
276 Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
277               565               570               575
278 Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
279       580               585               590
281 Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser
283       595       .       600               605
285 Ser Ser Ser Cys Ser Pro Pro Gln Lys Tyr Ala Gln Arg
287       610               615               620
288 <210> SEQ ID NO: 3
289 <211> LENGTH: 7789
290 <212> TYPE: DNA
291 <213> ORGANISM: Zea mays
293 <220> FEATURE:
294 <221> NAME/KEY: promoter
295 <222> LOCATION: (1)...(2715)
297 <221> NAME/KEY: 5'UTR
298 <222> LOCATION: (2716)...(2781)
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/047,593

DATE: 02/14/2002
TIME: 20:21:34

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\02142002\J047593.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

OIPE

```
        RAW SEQUENCE LISTING                      DATE: 02/07/2002
        PATENT APPLICATION:  US/10/047,593       TIME: 10:11:12

           Input Set : A:\1090D2SEQLIST.TXT
           Output Set: N:\CRF3\02072002\J047593.raw

     4 <110> APPLICANT: Crane, Edmund H. III
     5         Rice, Douglas A.
     7 <120> TITLE OF INVENTION: Maize NPR1 Polynucleotides and Methods
     8         of Use
    10 <130> FILE REFERENCE: 1090D2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/047,593
C--> 12 <141> CURRENT FILING DATE: 2002-01-15
    12 <150> PRIOR APPLICATION NUMBER: 60/130,692
    13 <151> PRIOR FILING DATE: 1999-04-23
    15 <150> PRIOR APPLICATION NUMBER: 09/551,778
    16 <151> PRIOR FILING DATE: 2000-04-18
    18 <160> NUMBER OF SEQ ID NOS: 6
    20 <170> SOFTWARE: FastSEQ for Windows Version 4.0


ERRORED SEQUENCES
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   200 <210> SEQ ID NO: 2
   201 <211> LENGTH: 621
   202 <212> TYPE: PRT
   203 <213> ORGANISM: Zea mays
   205 <400> SEQUENCE: 2
   206 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser Tyr Leu
   207  1               5                  10                  15
   208 Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro Gly Pro
   209              20                  25                  30
   210 Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly Gly Val
   211          35                  40                  45
   212 Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu Asn Arg
   213      50                  55                  60
   214 Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu Asp Cys
   215 65                  70                  75                  80
   216 Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
   217                  85                  90                  95
   218 His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
   219              100                 105                 110
   220 Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Ala Gly
   221          115                 120                 125
   222 Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
   223      130                 135                 140
   224 Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
   225 145                 150                 155                 160
   226 Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
```

```
227                 165                 170                 175
228 Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
229                 180                 185                 190
230 Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
231             195                 200                 205
232 Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
233         210                 215                 220
234 Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
235 225                 230                 235                 240
236 Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
237                 245                 250                 255
238 Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
239             260                 265                 270
240 Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln Thr Ala
241             275                 280                 285
242 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
243         290                 295                 300
244 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu
245 305                 310                 315                 320
246 Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala Leu His
247             325                 330                 335
248 Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp
249             340                 345                 350
250 Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
251         355                 360                 365
252 Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
253     370                 375                 380
254 Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
255 385                 390                 395                 400
256 Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
257             405                 410                 415
258 Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
259             420                 425                 430
260 Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
261         435                 440                 445
262 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
263     450                 455                 460
264 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
265 465                 470                 475                 480
266 Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
267                 485                 490                 495
268 Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
269             500                 505                 510
270 Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
271         515                 520                 525
272 Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
273     530                 535                 540
274 Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
275 545                 550                 555                 560
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RAW SEQUENCE LISTING   DATE: 02/07/2002
PATENT APPLICATION: US/10/047,593   TIME: 10:11:12

        Input Set : A:\1090D2SEQLIST.TXT
        Output Set: N:\CRF3\02072002\J047593.raw

    276 Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
    277   565   570   575
    278 Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
    279   580   585   590
E--> 280
Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser ⌐   595   600
    450 <210> SEQ ID NO: 4   insert hand return
    451 <211> LENGTH: 621
    452 <212> TYPE: PRT
    453 <213> ORGANISM: Zea mays
    455 <400> SEQUENCE: 4
    456 Met Glu Pro Ser Ser Ser Ile Thr Phe Ala Ser Ser Ser Ser Tyr Leu
    457 1   5   10   15
    458 Ser Asn Gly Ser Ser Pro Cys Ser Val Ala Leu Pro Pro Pro Gly Pro
    459   20   25   30
    460 Pro Gln Thr Pro Pro Leu Pro Ala Gly Gln Gly Trp Gly Gly Gly Val
    461   35   40   45
    462 Ala Ala Ala Gly Ser Gly Gly Ser Val Glu Ala Val Ser Leu Asn Arg
    463   50   55   60
    464 Leu Ser Lys Asn Leu Glu Arg Leu Leu Leu Asp Pro Asp Leu Asp Cys
    465 65   70   75   80
    466 Ser Asp Ala Asp Val Asp Val Pro Asp Gly Gly Pro Pro Val Pro Ile
    467   85   90   95
    468 His Arg Cys Ile Leu Ala Ala Arg Ser Asp Phe Phe Tyr Asp Leu Phe
    469   100   105   110
    470 Ala Ala Arg Gly Arg Ala Gly Ala Ala Arg Gly Asp Ala Ala Ala Gly
    471   115   120   125
    472 Ala Gly Val Ala Ala Glu Gly Ala Ala Ser Gly Arg Pro Arg Tyr Lys
    473   130   135   140
    474 Met Glu Asp Leu Val Pro Ala Gly Arg Val Gly Arg Glu Ala Phe Gln
    475 145   150   155   160
    476 Ala Phe Leu Gly Tyr Leu Tyr Thr Gly Lys Leu Arg Pro Ala Pro Val
    477   165   170   175
    478 Asp Val Val Ser Cys Ala Asp Pro Val Cys His His Asp Ser Cys Pro
    479   180   185   190
    480 Pro Ala Ile Arg Ser Ala Val Glu Leu Met Tyr Ala Ala Cys Thr Phe
    481   195   200   205
    482 Lys Ile Pro Glu Leu Thr Ser Leu Phe Gln Arg Arg Leu Leu Asn Phe
    483   210   215   220
    484 Val Asp Lys Thr Leu Val Glu Asp Val Ile Pro Ile Leu Glu Val Ala
    485 225   230   235   240
    486 Ser His Ser Gly Leu Thr Gln Val Ile Asp Lys Cys Ile Gln Arg Ile
    487   245   250   255
    488 Ala Arg Ser Asp Leu Asp Asp Ile Ser Leu Asp Lys Glu Leu Pro Pro
    489   260   265   270
    490 Glu Ala Val Asp Glu Ile Lys Asn Leu Arg Lys Lys Ser Gln Thr Ala
    491   275   280   285
    492 Asp Gly Asp Thr Phe Ile Ser Asp Pro Val His Glu Lys Arg Val Arg
    493   290   295   300
    494 Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Lys Leu

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/047,593

DATE: 02/07/2002
TIME: 10:11:12

Input Set : A:\1090D2SEQLIST.TXT
Output Set: N:\CRF3\02072002\J047593.raw

```
495 305                    310                 315                 320
496 Leu Leu Asn Glu Ser Asp Ile Thr Leu Asp Asp Ala Asn Ala Leu His
497                    325                 330                 335
498 Tyr Ala Ala Ser Tyr Cys Asp Pro Lys Val Val Ser Glu Leu Leu Asp
499                340                 345                 350
500 Leu Ala Met Ala Asn Leu Asn Leu Lys Asn Ser Arg Gly Tyr Thr Ala
501            355                 360                 365
502 Leu His Leu Ala Ala Met Arg Arg Glu Pro Ala Ile Ile Met Cys Leu
503        370                 375                 380
504 Leu Asn Lys Gly Ala Asn Val Ser Gln Leu Thr Ala Asp Gly Arg Ser
505 385                    390                 395                 400
506 Ala Ile Gly Ile Cys Arg Arg Leu Thr Arg Ala Lys Asp Tyr Asn Thr
507                    405                 410                 415
508 Lys Met Glu Gln Gly Gln Glu Ser Asn Lys Asp Arg Leu Cys Ile Asp
509                420                 425                 430
510 Ile Leu Glu Arg Glu Met Met Arg Asn Pro Met Ala Val Glu Asp Ala
511          435                 440                 445
512 Val Thr Ser Pro Leu Leu Ala Asp Asp Leu His Met Lys Leu Leu Tyr
513        450                 455                 460
514 Leu Glu Asn Arg Val Ala Phe Ala Arg Leu Phe Phe Pro Ala Glu Ala
515 465                    470                 475                 480
516 Lys Val Ala Met Gln Ile Ala Gln Ala Asp Thr Thr Glu Glu Phe Gly
517                    485                 490                 495
518 Gly Ile Val Ala Val Ala Ala Ser Thr Ser Gly Lys Leu Arg Glu Val
519                500                 505                 510
520 Asp Leu Asn Glu Thr Pro Val Thr Gln Asn Lys Arg Leu Arg Ser Arg
521          515                 520                 525
522 Val Asp Ala Leu Met Lys Thr Val Glu Leu Gly Arg Arg Tyr Phe Pro
523        530                 535                 540
524 Asn Cys Ser Gln Val Leu Asp Lys Phe Leu Glu Asp Asp Leu Pro Glu
525 545                    550                 555                 560
526 Gly Leu Asp Gln Phe Tyr Leu Gln Arg Gly Thr Ala Asp Glu Gln Lys
527                565                 570                 575
528 Val Lys Arg Met Arg Phe Cys Glu Leu Lys Glu Asp Val Leu Lys Ala
529                580                 585                 590
```

E--> 530

Phe Ser Lys Asp Lys Ala Glu Gly Ser Val Phe Ser Gly Leu Ser Ser   ↑   595   600

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533 <211> LENGTH: 2715
534 <212> TYPE: DNA
535 <213> ORGANISM: Zea mays
537 <220> FEATURE:
538 <221> NAME/KEY: promoter
539 <222> LOCATION: (1)...(2715)
541 <400> SEQUENCE: 5
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543 gaagccgacc gttggcgctt tggagccgtt ggcgcaccgg acactgtccg gtgcacaccg   120
544 gacagtcagg tgcccccttc cgaccgttgg ctcggccacg tgtttcgcgc ggatcgcgcg   180
545 gcagaccgtt ggcccgaccg accgttggct caccggacag tccggtgcac accagacagt   240
546 ccggtgaatt atagccgtac gccgttaatc acttcccgag agcagcaagt tcgcctgagc   300
```

```
547 cagcctggcg caccggacac tgtccggtga accaccggac agtccggtgc acccagtcag   360
548 agctgacttt ggctgaacaa agtcatcttt agttccaact tgattttttcc tgtttccagc   420
549 acttagacac aatacattag tctctaaaac aatgtattaa ttctgagaaa catacctta    480
550 tacttggttt gtactttgtc caccatttaa cacttgggca cttgtgttgg acactaaatc   540
551 accaaaatac ttagaaatgg cccaagggca catttccctt tcaacagtcc ggtgccacac   600
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553 ctatagcgtt ttgcagtcga ccgttggcgc acagagagcc attgctccgc tggctgaccg   720
554 gacagtccga tgaattatag cggascgcgc ctctgaattc ccgagtgtgg cctgtttgaa   780
555 gggcgcctgg cctggtgcac cgaacaatgt atggtgcgcc aaaaatcagc acactcaagt   840
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558 cgtcaactac taaaatctat ttatagaaag tggttaaccc tatttccctt tcagcacact  1020
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560 ggtcctcgac atgcaggacc ctaggccccg ttagaatggg gcttgtccat aagagagttg  1140
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562 tgttttgcca acatctgatg atatgtcttg gtgcttacaa aagccttgtt ttttatcttc  1260
563 ctttcgtctt aataaagatc catattacat ttatatttac tatgtcatat atatacctca  1320
564 ctatctcgaa gatacatctc gttgcggaag cataaggtag ctttggaggt aaagcttaga  1380
565 gcgacatgtg ggtgcaacaa acaaacatgg gggcacaaca cacctcacct catataacta  1440
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567 atcaaataca ccttcttaca caatttgtcc attttatatt tttcgtttcc aataacaaac  1560
568 tcaaagtgac ttgttttttt ggacctttga cacatagcct ttaaagtaga tttcacaatt  1620
569 taagcttgtt atgtaaaaca aactaatttc gagagaggct gattgaggag aaagtctgcg  1680
570 gtcgatgatt caattggacg aaatcgatgt ttaaactgtc ttgttgatta aatttctagc  1740
571 ttcacacgtg cttgaacggc gtaggaagtg ttggaatttc ccttcttatg atttattaga  1800
572 gtagagtttt gttacagttt atttacggat tcattacggt atttattagg gatacgttga  1860
573 catataactt cagtctttct tttttaatag tcacaagaaa ctttcacaca cctactagga  1920
574 gtaacagaaa aacatggaca tattgatttt tgaaaaaaga aatattgaca gataaggtgt  1980
575 tggggaccgt agagactaga gaggatgagg acgacgccag gcagacgagc cttgccgatt  2040
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578 tctattctcc ttccggcgcc tctctagtct attctccttc ctcgtcgagt cgtcgtcttc  2220
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583 catatttct gttcctggcc tgacgcagcg ccggtgagat ttcagtccgg gatcggcaac  2520
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E--> 585

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VERIFICATION SUMMARY   DATE: 02/07/2002
PATENT APPLICATION: US/10/047,593   TIME: 10:11:13

Input Set : A:\1090D2SEQLIST.TXT
Output Set: N:\CRF3\02072002\J047593.raw

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L:12  M:270 C: Current Application Number differs, Replaced Current Application No
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:280 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:2
L:280 M:252 E: No. of Seq. differs, <211>LENGTH:Input:621 Found:592 SEQ:2
L:530 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:4
L:530 M:252 E: No. of Seq. differs, <211>LENGTH:Input:621 Found:592 SEQ:4
L:585 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:5
L:585 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:585 M:252 E: No. of Seq. differs, <211>LENGTH:Input:2715 Found:2580 SEQ:5
```